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TECH CENTER 1600/2900



- 1 -

SEQUENCE LISTING

<110> Vertino, Paula M.

<120> TMS1 Compositions and Methods of Use

<130> E0355/7003/ERG/MAT

<140> US 09/691,763

<141> 2000-10-18

<150> US 60/159,975

<151> 1999-10-18

<160> 27

<170> FastSEQ for Windows Version 3.0

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<212> DNA

<213> Homo Sapiens

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83
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<213> Homo Sapiens

<220>
<221> CDS
<222> (75) . . . (662)

<400> 2

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          1           5           10

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 Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu
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 Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu
 30 35 40

ctg tcc atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac
 Leu Ser Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr
 45 50 55 60

ctg gag acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg
 Leu Glu Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met
 65 70 75

tct gga gcc gcg cca gct ggg atc cag gcc cct cct cag tcg gca gcc 398
 Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala
 95 100 105

aag cca ggc ctg cac ttt ata gac cag cac cg_g gct gcg ctt atc gc_g 446
Lys Pro Gly Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala
110 115 120

agg gtc aca aac gtt gag tgg ctg ctg gat gct ctg tac ggg aag gtc 494
 Arg Val Thr Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val

125

130

135

140

ctg acg gat gag cag tac cag gca gtg cg^g gcc gag ccc acc aac cca
Leu Thr Asp Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro
145 150 155

542

agc aag atg cgg aag ctc ttc agt ttc aca cca gcc tgg aac tgg acc
Ser Lys Met Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr
160 165 170

590

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Cys Lys Asp Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu
175 180 185

638

gtg gag gac ctg gag cgg agc tga ggctccttcc cagcaacact ccggtcagcc
Val Glu Asp Leu Glu Arg Ser *
190 195

692

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cagcttgaaa aaaaaaaaaa

752

770

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<210> 3
<211> 195
<212> PRT
<213> Homo Sapiens

<400> 3

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35 40 45
Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr
50 55 60
Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu
65 70 75 80
Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Ser Gly Ala Ala
85 90 95
Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro Gly Leu
100 105 110
His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn
115 120 125
Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu
130 135 140
Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg
145 150 155 160
Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu
165 170 175
Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu
180 185 190

Glu Arg Ser
195

<210> 4
<211> 626
<212> DNA
<213> Homo Sapiens

<400> 4

85

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gggtgagcgg cggcagcggc cggggatcct ggagccatgg ggcgcgcgcg cgacgcccac 180
ctggatgcgc tggagaacct gaccggccgag gagctcaaga agttcaagct gaagctgctg 240
tcggtgccgc tgccgcgaggc ctacgggcgc atccccggg gcgcgctgt gtccatggac 300
gccttggacc tcaccgacaa gctggtcage ttctacctgg agacctacgg cgccgagctc 360
accgctaacg tgctgcgca catgggcctg caggagatgg ccgggcagct gcaggcggcc 420
acgcaccagg gtgagccccc cccgttcccc tccacccctg cttttccctc caccacacc 480
agcgcttacc ccgcggggtc ttccgcttcc tggccttcc acccctaaac aaagctgctc 540
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gggaagggaa gggaaagggaa tcactt 626

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<211> 340
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (67)...(339)

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Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn
1 5 10

ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg tcg gtg 156
Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val
15 20 25 30

ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg ctg tcc 204
Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser
35 40 45

atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac ctg gag 252
Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu
50 55 60

acc tac ggc gcc gag ctc acc gct aac gtc ctg cgc gac atg ggc ctg 300
Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu
65 70 75

cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag g 340
Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln
80 85 90

<210> 6
<211> 91
<212> PRT
<213> Homo Sapiens

<400> 6

Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr
1 5 10 15
Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu
20 25 30
Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp
35 40 45

66

C

Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr
50 55 60
Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu
65 70 75 80
Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln
85 90

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<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (3)...(56)

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Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala
1 5 10 15

gcc aag cca g 57
Ala Lys Pro

11

<210> 8
<211> 18
<212> PRT
<213> Homo Sapiens

<400> 8
Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala
1 5 10 15
Lys Pro

<210> 9
<211> 356
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (3)...(258)

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gc ctg cac ttt ata gac cag cac cgg gct gcg ctt atc gcg agg gtc 47
Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val
1 5 10 15

aca aac gtt gag tgg ctg ctg gat gct ctg tac ggg aag gtc ctg acg 95
Thr Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr
20 25 30

gat gag cag tac cag gca gtg cgg gcc gag ccc acc aac cca agc aag 143
Asp Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys
35 40 45

atg cgg aag ctc ttc agt ttc aca cca gcc tgg aac tgg acc tgc aag 191

67

67

Met Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys
50 55 60

gac ttg ctc ctc cag gcc cta agg gag tcc cag tac ctg gtg gag 239
Asp Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu
65 70 75

gac ctg gag cggttcc gctccttccc agcaacactc cggtcagccc 288
Asp Leu Glu Arg Ser *
80

ctggcaatcc caccaaata tcctgaatct gatctttta tacacaatat acgaaaagcc 348
agcttgaa 356

<210> 10
<211> 84
<212> PRT
<213> Homo Sapiens

<400> 10

Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr
1 5 10 15

Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp
20 25 30

Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met
35 40 45

Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp
50 55 60

Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp
65 70 75 80

Leu Glu Arg Ser

<210> 11
<211> 18
<212> DNA
<213> Homo Sapiens

<400> 11

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<210> 12
<211> 18
<212> DNA
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<400> 12

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<210> 13
<211> 17
<212> DNA
<213> Homo Sapiens

<400> 13

tgggcctgca ggagatg 17

<210> 14
<211> 22
<212> DNA

<213> Homo Sapiens
<400> 14
ccttcctggg catggaggcc tg 22

<210> 15
<211> 21
<212> DNA
<213> Homo Sapiens

<400> 15
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<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Primer

<400> 16
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<210> 17
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Primer

<400> 17
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<210> 18
<211> 19
<212> DNA
<213> Homo Sapiens

<400> 18
ttgttagcggg gtgagcggc 19

<210> 19
<211> 22
<212> DNA
<213> Homo Sapiens

<400> 19
aacgtccata aacaacaacg cg 22

<210> 20
<211> 803
<212> DNA
<213> Mus Musculus

<220>
<221> CDS
<222> (162) ... (743)

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agcaagagta aaaggtgacc gcggctgccc accccagagc c atg ggg cgg gca cga 176
Met Gly Arg Ala Arg
1 5

gat gcc atc ctg gac gct ctt gaa aac ttg tca ggg gat gaa ctc aaa 224
Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Ser Gly Asp Glu Leu Lys
10 15 20

aag ttc aag atg aag ctg ctg aca gtg caa ctg cga gaa ggc tat ggg 272
Lys Phe Lys Met Lys Leu Leu Thr Val Gln Leu Arg Glu Gly Tyr Gly
25 30 35

cgc atc cca cgc ggg gcc ctg ctg cag atg gac gcc ata gat ctc act 320
Arg Ile Pro Arg Gly Ala Leu Leu Gln Met Asp Ala Ile Asp Leu Thr
40 45 50

gac aaa ctt gtc agc tac tat ctg gag tcg tat ggc ttg gag ctc aca 368
Asp Lys Leu Val Ser Tyr Tyr Leu Glu Ser Tyr Gly Leu Glu Leu Thr
55 60 65

atg act gtg ctt aga gac atg ggc tta cag gag ctg gct gag cag ctg 416
Met Thr Val Leu Arg Asp Met Gly Leu Gln Glu Leu Ala Glu Gln Leu
70 75 80 85

caa acg act aaa gaa gag tct gga gct gtg gca gct gca gcc agt gtc 464
Gln Thr Thr Lys Glu Glu Ser Gly Ala Val Ala Ala Ala Ser Val
90 95 100

cct gct cag agt aca gcc aga aca gga cac ttt gtg gac cag cac agg 512
Pro Ala Gln Ser Thr Ala Arg Thr Gly His Phe Val Asp Gln His Arg
105 110 115

caa gca ctc att gcc agg gtc aca gaa gtg gac gga gtg ctg gat gct 560
Gln Ala Leu Ile Ala Arg Val Thr Glu Val Asp Gly Val Leu Asp Ala
120 125 130

ttg cat ggc agt gtg ctg act gaa gga cag tac cag gca gtt cgt gca 608
Leu His Gly Ser Val Leu Thr Glu Gly Gln Tyr Gln Ala Val Arg Ala
135 140 145

gag acc acc agc caa gac aag atg agg aag ctc ttc agc ttt gtt cca 656
Glu Thr Thr Ser Gln Asp Lys Met Arg Lys Leu Phe Ser Phe Val Pro
150 155 160 165

tcc tgg aac ctg acc tgc aag gac tcc ctc ctc cag gcc ttg aag gaa 704
Ser Trp Asn Leu Thr Cys Lys Asp Ser Leu Leu Gln Ala Leu Lys Glu
170 175 180

ata cat ccc tac ttg gtg atg gac ctg gag cag agc tga ggtatctttt 753
Ile His Pro Tyr Leu Val Met Asp Leu Glu Gln Ser *
185 190

ccagctacat tatcttagctc ctgactttgt atacacaatt tttgaaaaaaaa 803

<210> 21
<211> 193
<212> PRT

<213> Mus Musculus

C/

<400> 21
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Ser
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20 25 30
Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Gln Met Asp
35 40 45
Ala Ile Asp Leu Thr Asp Lys Leu Val Ser Tyr Tyr Leu Glu Ser Tyr
50 55 60
Gly Leu Glu Leu Thr Met Thr Val Leu Arg Asp Met Gly Leu Gln Glu
65 70 75 80
Leu Ala Glu Gln Leu Gln Thr Thr Lys Glu Glu Ser Gly Ala Val Ala
85 90 95
Ala Ala Ala Ser Val Pro Ala Gln Ser Thr Ala Arg Thr Gly His Phe
100 105 110
Val Asp Gln His Arg Gln Ala Leu Ile Ala Arg Val Thr Glu Val Asp
115 120 125
Gly Val Leu Asp Ala Leu His Gly Ser Val Leu Thr Glu Gly Gln Tyr
130 135 140
Gln Ala Val Arg Ala Glu Thr Thr Ser Gln Asp Lys Met Arg Lys Leu
145 150 155 160
Phe Ser Phe Val Pro Ser Trp Asn Leu Thr Cys Lys Asp Ser Leu Leu
165 170 175
Gln Ala Leu Lys Glu Ile His Pro Tyr Leu Val Met Asp Leu Glu Gln
180 185 190
Ser

<210> 22
<211> 605
<212> DNA
<213> Rattus Norvegicus

<220>
<221> CDS
<222> (2)...(518)

<220>
<221> Variant
<222> (109)...(109)
<223> y = C or T/U

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Phe Lys Ile Lys Leu Leu Thr Ala Pro Val Arg Glu Gly Tyr Gly Arg
1 5 10 15
atc cca cgg ggg gcc ctg ctg cag atg gac ccc ata gac ctc act gat 97
Ile Pro Arg Gly Ala Leu Leu Gln Met Asp Pro Ile Asp Leu Thr Asp
20 25 30
aaa ctc gtc agy tac tat ctg gag ggg tat ggc ttg gag ctc aca atg 145
Lys Leu Val Xaa Tyr Tyr Leu Glu Gly Tyr Gly Leu Glu Leu Thr Met
35 40 45
act gtg ctt aga gac atg ggc ata cag gag ctg gct gag cag ctg caa 193
C/

Thr Val Leu Arg Asp Met Gly Ile Gln Glu Leu Ala Glu Gln Leu Gln
50 55 60

aag att atg gaa gag tct gga gct gtg gct act gca acc agt gtc cct 241
Lys Ile Met Glu Glu Ser Gly Ala Val Ala Thr Ala Thr Ser Val Pro
65 70 75 80

gct cag ggc aca gcc aga aca gaa cat ttt gtg gac caa cac agg caa 289
Ala Gln Gly Thr Ala Arg Thr Glu His Phe Val Asp Gln His Arg Gln
85 90 95

gca ctc att gcc agg gtc aca gaa gtt gat ggt ttg ctg gat gct ctg 337
Ala Leu Ile Ala Arg Val Thr Glu Val Asp Gly Leu Leu Asp Ala Leu
100 105 110

tat ggc aat gtg ctg act gaa gga cag tac cag gca gtt cgt gca gag 385
Tyr Gly Asn Val Leu Thr Glu Gly Gln Tyr Gln Ala Val Arg Ala Glu
115 120 125

acc acc aac caa aac aag atg agg aag ctc ttt agc ttt gct cca gcc 433
Thr Thr Asn Gln Asn Lys Met Arg Lys Leu Phe Ser Phe Ala Pro Ala
130 135 140

tgg aac ctg acc tgc aag aac ttg ttc ctt gag gcc ttg agg caa aca 481
Trp Asn Leu Thr Cys Lys Asn Leu Phe Leu Glu Ala Leu Arg Gln Thr
145 150 155 160

cag ccc tac ttg gtg aca gac ctg gaa cag agc tga g gtatctttc 528
Gln Pro Tyr Leu Val Thr Asp Leu Glu Gln Ser *
165 170

cagctacaca tcttagctcct ggttttgtat aaaaaatttt ctaaaaacaa gtttgtat 588
gtgtttctc gaaaaaa 605

<210> 23
<211> 171
<212> PRT
<213> Rattus Norvegicus

<220>
<221> Unknown
<222> (36)...(36)
<223> Xaa can be any amino acid.

<400> 23
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1 5 10 15
Ile Pro Arg Gly Ala Leu Leu Gln Met Asp Pro Ile Asp Leu Thr Asp
20 25 30
Lys Leu Val Xaa Tyr Tyr Leu Glu Gly Tyr Gly Leu Glu Leu Thr Met
35 40 45
Thr Val Leu Arg Asp Met Gly Ile Gln Glu Leu Ala Glu Gln Leu Gln
50 55 60
Lys Ile Met Glu Glu Ser Gly Ala Val Ala Thr Ala Thr Ser Val Pro
65 70 75 80
Ala Gln Gly Thr Ala Arg Thr Glu His Phe Val Asp Gln His Arg Gln
85 90 95
Ala Leu Ile Ala Arg Val Thr Glu Val Asp Gly Leu Leu Asp Ala Leu
100 105 110
Tyr Gly Asn Val Leu Thr Glu Gly Gln Ala Val Arg Ala Glu

9.2

C

115	120	125
Thr Thr Asn Gln Asn Lys Met Arg Lys Leu Phe Ser Phe Ala Pro Ala		
130	135	140
Trp Asn Leu Thr Cys Lys Asn Leu Phe Leu Glu Ala Leu Arg Gln Thr		
145	150	155
Gln Pro Tyr Leu Val Thr Asp Leu Glu Gln Ser		
165	170	

<210> 24
<211> 713
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (75)...(605)

<400> 24

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Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu
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Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu
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Leu Ser Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr
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Leu His Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr
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Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met
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Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp
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Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp
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Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Leu His Phe Ile
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Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn Val Glu Trp
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Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu Gln Tyr Gln
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1 5 10

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Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu
15 20 25

tcg gtg ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg 206
Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu
C
9/

30	35	40	
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ctg gag acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg Leu Glu Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met 65	70	75	302
ggc ctg cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag ggc Gly Leu Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly 80	85	90	350
tct gga gcc gcg cca gct ggg atc cag gcc cct cct cag tcg gca gcc Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala 95	100	105	398
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95